

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/533,144
Source: PG
Date Processed by STIC: 6/30/06

ENTERED



PCT

RAW SEQUENCE LISTING DATE: 06/30/2006
 PATENT APPLICATION: US/10/533,144 TIME: 08:47:13

Input Set : F:\seqlist.txt
 Output Set: N:\CRF4\06302006\J533144.raw

4 <110> APPLICANT: MASUDA, ESTEBAN
 6 <120> TITLE OF INVENTION: METHODS OF SCREENING CYCLIC PEPTIDES AND
 7 IDENTIFYING TARGETS THEREFOR
 10 <130> FILE REFERENCE: RIGL-023
 12 <140> CURRENT APPLICATION NUMBER: 10/533,144
 13 <141> CURRENT FILING DATE: 2005-04-27
 15 <150> PRIOR APPLICATION NUMBER: US03/27370
 16 <151> PRIOR FILING DATE: 2003-08-30
 18 <150> PRIOR APPLICATION NUMBER: 60/407,385
 19 <151> PRIOR FILING DATE: 2002-08-30
 21 <160> NUMBER OF SEQ ID NOS: 2
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1227
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: recombinant polynucleotide
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (1)...(1227)
 37 <220> FEATURE:
 38 <221> NAME/KEY: misc_feature
 39 <222> LOCATION: 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171
 40 <223> OTHER INFORMATION: n = A,T,C or G
 43 <400> SEQUENCE: 1
 44 atg gag agc ggc agc ccc gag atc gag aag ctg agt cag agc gac atc 48
 45 Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
 46 1 5 10 15
 48 tac tgg gac agc atg gtg agc atc acc gag acc ggc gtg gag gag gtg 96
 49 Tyr Trp Asp Ser Met Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
 50 20 25 30
 52 ttc gac ctg acc gtg ccc ggc ccc cac aac ttc gtg gcc aac gac atc 144
 53 Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
 54 35 40 45
 W--> 56 atc gtc cac aac agc nnn nnn nnn nnn tgc atc agc ggc gac agc ctg 192
 57 Ile Val His Asn Ser Xaa Xaa Xaa Xaa Cys Ile Ser Gly Asp Ser Leu
 58 50 55 60
 60 atc agc ctg gcc agc acc ggc aag agg gtg agc atc aag gac ctg ctg 240
 61 Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu
 62 65 70 75 80
 64 gac gag aag gac ttc gag atc tgg gcc atc aac gag cag acc atg aag 288
 65 Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys

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66		85		90		95		
68	cta gag agc gcc aag gtg agc agg gtg ttc tgc acc ggc aag aag cta	336						
69	Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu							
70		100		105		110		
72	gtg tac atc cta aga acc agg cta ggc agg acc atc aag gcc acc gcc	384						
73	Val Tyr Ile Leu Arg Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala							
74		115		120		125		
76	aac cac agg ttc cta acc atc gac ggc tgg aag agg cta gac gag cta	432						
77	Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu							
78		130		135		140		
80	agc cta aag gag cac atc gcc cta ccc cgg aag cta gag agc agc agc	480						
81	Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser							
82	145		150		155		160	
84	cta cag cta ggc ctc cgc ggc cag atc gat gtg agc aag ggc gag gag	528						
85	Leu Gln Leu Gly Leu Arg Gly Gln Ile Asp Val Ser Lys Gly Glu Glu							
86		165		170		175		
88	ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta	576						
89	Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val							
90		180		185		190		
92	aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc	624						
93	Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr							
94		195		200		205		
96	tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	672						
97	Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro							
98		210		215		220		
100	gtg ccc tgg ccc acc ctc gtg acc acc ctg acc cac ggc gtg cag tgc	720						
101	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val Gln Cys							
102	225		230		235		240	
104	ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc ttc aag tcc	768						
105	Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser							
106		245		250		255		
108	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	816						
109	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp							
110		260		265		270		
112	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	864						
113	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr							
114		275		280		285		
116	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	912						
117	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly							
118		290		295		300		
120	aac atc ctg ggg cac aag ctt gag tac aac ttc aac agc cac aac gtg	960						
121	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val							
122	305		310		315		320	
124	tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	1008						
125	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys							
126		325		330		335		
128	atc cgc cac aac atc gag gac gga tcc gtg cag ctc gcc gac cac tac	1056						
129	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr							
130		340		345		350		

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```

132 cag cag aac acc cca att ggc gac ggg ccc gtg ctg ctg ccc gac aac 1104
133 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
134      355      360      365
136 cac tac ctg agc acc cag agc gct ctt tcg aaa gac ccc aac gag aag 1152
137 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
138      370      375      380
140 cgc gat cat atg gtc ctg ctc gag ttc gtg acc gcc gcc ggg atc act 1200
141 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
142 385      390      395      400
144 ctc ggc atg gac gag ctg tac aag taa 1227
145 Leu Gly Met Asp Glu Leu Tyr Lys *
146      405
149 <210> SEQ ID NO: 2
150 <211> LENGTH: 408
151 <212> TYPE: PRT
152 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <221> NAME/KEY: VARIANT
156 <222> LOCATION: 54, 55, 56, 57
157 <223> OTHER INFORMATION: Xaa = Any Amino Acid
159 <220> FEATURE:
160 <223> OTHER INFORMATION: recombinant polypeptide
162 <400> SEQUENCE: 2
163 Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
164 1      5      10      15
165 Tyr Trp Asp Ser Met Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
166      20      25      30
167 Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
168      35      40      45
W--> 169 Ile Val His Asn Ser Xaa Xaa Xaa Xaa Cys Ile Ser Gly Asp Ser Leu
170      50      55      60
171 Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu
172 65      70      75      80
173 Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys
174      85      90      95
175 Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu
176      100     105     110
177 Val Tyr Ile Leu Arg Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala
178      115     120     125
179 Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu
180      130     135     140
181 Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser
182 145      150     155     160
183 Leu Gln Leu Gly Leu Arg Gly Gln Ile Asp Val Ser Lys Gly Glu Glu
184      165     170     175
185 Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
186      180     185     190
187 Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
188      195     200     205

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```

189 Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
190      210                      215                      220
191 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val Gln Cys
192 225                      230                      235                      240
193 Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser
194      245                      250                      255
195 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
196      260                      265                      270
197 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
198      275                      280                      285
199 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
200      290                      295                      300
201 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val
202 305                      310                      315                      320
203 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
204      325                      330                      335
205 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
206      340                      345                      350
207 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
208      355                      360                      365
209 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
210      370                      375                      380
211 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
212 385                      390                      395                      400
213 Leu Gly Met Asp Glu Leu Tyr Lys
214      405

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/533,144

DATE: 06/30/2006
TIME: 08:47:14

Input Set : F:\seqlist.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 160,161,162,163,164,165,166,167,168,169,170,171

Seq#:1; Xaa Pos. 54,55,56,57

Seq#:2; Xaa Pos. 54,55,56,57

VERIFICATION SUMMARY

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Input Set : F:\seqlist.txt

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L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:144

M:341 Repeated in SeqNo=1

L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:48